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NOV 29 2000

SEQUENCE LISTING

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Adler, Jon Elliot
Lindemeier, Juergen
The Regents of the University of California

TECH CENTER 1600/2900

<120> Assays for Sensory Modulators Using a Sensory Cell
Specific G-Protein Beta Subunit

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<130> 02307E-092710US

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<140> US 09/492,029

<141> 2000-01-26

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<150> US 60/117,404

<151> 1999-01-27

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<170> PatentIn Ver. 2.1

DEC 04 2000

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TECH CENTER 1600/2900

<211> 156

<212> DNA

<213> Rattus sp.

<220>

<223> rat tongue circumvallate papillae taste receptor
cell cDNA clone 165-17

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<212> DNA

<213> Rattus sp.

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<221> CDS

<222> (78)..(2000)

<223> rat taste cell specific G-protein beta 3 subunit
(TC-Gbeta3)

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cccttgacct gtgaacc atg ggg gag atg gag cag ctg aag cag gag gcg 110
Met Gly Glu Met Glu Gln Leu Lys Gln Glu Ala
1 5 10

gag cag ctc aag aag cag att gct gat gcc agg aaa gcc tgt gcg gac 158
Glu Gln Leu Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp
15 20 25

atc act ctg gct gag ctt gtg tct ggc ctg gag gtg gtg gga cga gtc 206
 Ile Thr Leu Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val
 30 35 40

cag atg cg^g aca cg^g agg acg tta agg gga cac ctg gct aag atc tat 254
 Gln Met Arg Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr
 45 50 55

gcc atg cac tgg gcc act gac tct aag ctg cta gta agt gcc tcg cag 302
 Ala Met His Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln
 60 65 70 75

gat ggg aag ctg atc gtg tgg gac act tac acc acc aat aag gtg cat 350
 Asp Gly Lys Leu Ile Val Trp Asp Thr Tyr Thr Thr Asn Lys Val His
 80 85 90

gct atc ccg ctg cgt tcc tcc tgg gtc atg acc tgt gcc tat gca cca 398
 Ala Ile Pro Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro
 95 100 105

tca ggg aac ttc gtg gca tgt ggg ggg cta gat aac atg tgc tca atc 446
 Ser Gly Asn Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile
 110 115 120

tac agc ctc aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gaa ctc 494
 Tyr Ser Leu Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu
 125 130 135

tcg gct cac aca ggt tat ctc tcc tgt tgc cgc ttc ctg gat gac aac 542
 Ser Ala His Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn
 140 145 150 155

aac att gtg act agc tct ggg gac acc acg tgt gcc ttg tgg gac att 590
 Asn Ile Val Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile
 160 165 170

gag acg ggg cag cag aag aca gtg ttc gtg gga cac act ggt gac tgc 638
 Glu Thr Gly Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys
 175 180 185

atg agc ctg gct gtg tcc cca gac tac aaa ctc ttc atc tcg gga gct 686
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tgt gat gcc agc gcc aag ctc tgg gat gtg agg gaa ggg acc tgt cgc 734
 Cys Asp Ala Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg
 205 210 215

cag act ttc act ggc cac gag tca gac atc aat gct atc tgt ttc ttt 782
 Gln Thr Phe Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe
 220 225 230 235

ccc aat ggg gag gcc atc tgc act ggc tca gat gat gcc tcc tgc cgc 830
 Pro Asn Gly Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg
 240 245 250

ctc ttt gac ctg agg gca gac cag gaa ctg aca gcc tac tcc cac gag 878
 Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu
 255 260 265

agc atc atc tgt ggc atc acg tcc gta gcc ttc tca ctc agt ggt cg 926
 Ser Ile Ile Cys Gly Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg
 270 275 280

ctg ctc ttt gct ggc tat gat gac ttc aac tgc aat gtc tgg gac tct 974
 Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
 285 290 295

ctg aag tgt gag cgt gta ggc gtt ctt tct ggc cat gac aac aga gtc 1022
 Leu Lys Cys Glu Arg Val Gly Val Leu Ser Gly His Asp Asn Arg Val
 300 305 310 315

agt tgc ctg ggg gtc aca gct gac ggc atg gct gtg gcc act gga tcc 1070
 Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser
 320 325 330

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 Trp Asp Ser Phe Leu Lys Ile Trp Asn
 335 340

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 <213> Rattus sp.

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Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
 35 40 45

Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
 50 55 60

Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
 65 70 75 80

Val Trp Asp Thr Tyr Thr Asn Lys Val His Ala Ile Pro Leu Arg
 85 90 95

Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
 100 105 110

Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Ser Leu Lys Ser
 115 120 125
 Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
 130 135 140
 Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
 145 150 155 160
 Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
 165 170 175
 Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
 180 185 190
 Ser Pro Asp Tyr Lys Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
 195 200 205
 Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
 210 215 220
 His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
 225 230 235 240
 Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
 245 250 255
 Ala Asp Gln Glu Leu Thr Ala Tyr Ser His Glu Ser Ile Ile Cys Gly
 260 265 270
 Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
 275 280 285
 Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Leu Lys Cys Glu Arg
 290 295 300
 Val Gly Val Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
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 325 330 335
 Lys Ile Trp Asn
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 <211> 1523
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> (7)..(1029)
 <223> human taste cell specific G-protein beta 3 subunit

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 Lys Lys Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu
 15 20 25 30

gca gag ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cg 144
 Ala Glu Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg
 35 40 45

acg cgg cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac 192
 Thr Arg Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His
 50 55 60

tgg gcc act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag 240
 Trp Ala Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys
 65 70 75

ctg atc gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca 288
 Leu Ile Val Trp Asp Ser Tyr Thr Asn Lys Val His Ala Ile Pro
 80 85 90

ctg cgc tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac 336
 Leu Arg Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn
 95 100 105 110

ttt gtg gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc 384
 Phe Val Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu
 115 120 125

aaa tcc cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac 432
 Lys Ser Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His
 130 135 140

aca ggt tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg 480
 Thr Gly Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val
 145 150 155

acc agc tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg 528
 Thr Ser Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly
 160 165 170

cag cag aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg 576
 Gln Gln Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu
 175 180 185 190

gct gtg tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc 624
 Ala Val Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala
 195 200 205

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 Ser Ala Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe
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 Thr Gly His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly
 225 230 235

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 Glu Ala Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp
 240 245 250

a
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260																
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Cys	Gly	Ile	Thr	Ser	Val	Ala	Phe	Ser	Leu	Ser	Gly	Arg	Leu	Leu	Phe	
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Ala	Gly	Tyr	Asp	Asp	Phe	Asn	Cys	Asn	Val	Trp	Asp	Ser	Met	Lys	Ser	
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295																
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Glu	Arg	Val	Gly	Ile	Leu	Ser	Gly	His	Asp	Asn	Arg	Val	Ser	Cys	Leu	
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310																
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Gly	Val	Thr	Ala	Asp	Gly	Met	Ala	Val	Ala	Thr	Gly	Ser	Trp	Asp	Ser	
320															330	
325																
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Phe	Leu	Lys	Ile	Trp	Asn											
335																
340																
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atccgggtg	ccattccac	taagcttct	ccttgaggg	cagtggggag	catgggactg											
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gccttccctc	ccacagtc	tcacagcctc	tcccttaatg	agcaaggaca	acctgccc											1296
ccccagccct	ttgcaggccc	agcagactg	agtctgaggg	cccaggcc	aggattcctc											1356
ccccagagcc	actaccttg	tccaggcctg	ggtggatag	ggcggttggc	cctgtgacta											1416
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<211> 340

<212> PRT

<213> Homo sapiens

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Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg
35 40 45

Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala
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Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile
65 70 75 80

Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg
85 90 95

Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val
100 105 110

Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser
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Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly
130 135 140

Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser
145 150 155 160

Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
165 170 175

Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
180 185 190

Ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
195 200 205

Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
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His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Pro Asn Gly Glu Ala
225 230 235 240

Ile Cys Thr Gly Ser Asp Asp Ala Ser Cys Arg Leu Phe Asp Leu Arg
245 250 255

Ala Asp Gln Glu Leu Ile Cys Phe Ser His Glu Ser Ile Ile Cys Gly
260 265 270

Ile Thr Ser Val Ala Phe Ser Leu Ser Gly Arg Leu Leu Phe Ala Gly
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Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser Met Lys Ser Glu Arg
290 295 300

Val Gly Ile Leu Ser Gly His Asp Asn Arg Val Ser Cys Leu Gly Val
305 310 315 320

Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser Trp Asp Ser Phe Leu
325 330 335

Lys Ile Trp Asn
340